AMENDMENTS TO THE CLAIMS

Listing of Claims:

This Listing of Claims will replace all prior versions, and listings, of claims in the application:

1-45 (Cancelled)

46. (Currently amended) A method for sequencing nucleic acid, comprising:

a) attaching a template nucleic acid molecule having from about 10 to approximately 100,000 nucleotides in length to a cantilever suitable for detecting a mass dependent property associated with the cantilever, resulting in forming an attached template nucleic acid; wherein the attached template nucleic acid is partially double stranded prior to, concurrent with or subsequent to the attaching of the template nucleic acid;

b) contacting the attached template nucleic acid molecule with at least one type of a complimentary nucleotide structurally suitable for mass labeling; wherein the complimentary nucleotide comprises a 3' blocking or protecting group;

c) incubating the attached template nucleic acid molecule and the complimentary nucleotide under conditions suitable for incorporating the complimentary nucleotide to the attached template nucleic acid in a position complementary to a nucleotide in the attached template nucleic acid, wherein the complimentary nucleotide incorporated in the attached template nucleic acid is mass labeled prior to, concurrent with, or subsequent to the incorporation, yet prior to the addition of a next complimentary nucleotide; wherein complimentary nucleotides of different types have different mass labels that are attached to the complimentary nucleotides throughout a plurality of

cycles of said method for sequencing nucleic acid; and

d) identifying the complimentary nucleotide incorporated in the attached template nucleic acid by detecting a change in the mass dependent property associated with the cantilever, wherein the change is indicative of the incorporation of the complimentary nucleotide in the attached template nucleic acid.

47. (Previously presented) The method of claim 46, wherein the complimentary nucleotide comprises a chemical structure selected from the group consisting of deoxyadenosine 5' triphosphate (dATP), deoxythymidine 5' triphosphate (dTTP), deoxyguanosine 5' triphosphate (dGTP) and deoxycytosine 5' triphosphate (dCTP).

48. (Previously presented) The method of claim 46, wherein the complimentary nucleotide comprises a chemical structure selected from the group consisting of adenosine 5' triphosphate (ATP), thymidine 5' triphosphate (TTP), guanosine 5' triphosphate (GTP) and cytosine 5' triphosphate (CTP).

49. (Previously presented) The method of claim 46, wherein the change in the mass dependent property of the structure is determined by detecting deflection and/or resonant frequency shifts in the cantilever.

50. (Previously presented) The method of claim 49, wherein the deflection and/or

resonant frequency shift is detected by optical beam detection, piezoelectric detection, piezoresistance detection or electrical resistance detection.

51. (Previously presented) The method of claim 46, wherein a single nucleotide polymorphism (SNP) is identified.

52. (Previously presented) The method of claim 46, further comprising iteratively repeating parts b) through d), wherein for each iteration the attached template is contacted with a different type of complimentary nucleotide.

53. (Previously presented) The method of claim 46, further comprising hybridizing a primer to the attached template nucleic acid.

54. (Previously presented) The method of claim 53, wherein the labeled nucleotides are covalently attached to the 3' end of the primer by a polymerase.

55. (Previously presented) The method of claim 46, wherein the method comprises a plurality of cantilevers, the cantilevers being arranged in a selected pattern.

56. (Currently amended) A method for sequencing nucleic acid, comprising:

a) attaching a template nucleic acid molecule having from about 10 to approximately 100,000 nucleotides in length to a cantilever suitable for detecting a mass dependent property

associated with the cantilever, resulting in forming an attached template nucleic acid; wherein the attached template nucleic acid is partially double stranded prior to, concurrent with or subsequent to the attaching of the template nucleic acid;

b) contacting the attached template nucleic acid molecule with a first type of complimentary nucleotide structurally suitable for mass labeling, a second type of complimentary nucleotide structurally suitable for mass labeling, a third type of complimentary nucleotide structurally suitable for mass labeling, and a fourth type of complimentary nucleotide structurally suitable for mass labeling; wherein the first, second, third and fourth types of complimentary nucleotides comprise a 3' blocking or protecting group;

c) incubating the attached template nucleic acid molecule and the first, second, third and fourth types of complimentary nucleotides under conditions suitable for incorporating the first type of complimentary nucleotide to the attached template nucleic acid in a position complementary to a nucleotide in the attached template nucleic acid, wherein the first type of complimentary nucleotide incorporated in the attached template nucleic acid is mass labeled prior to, concurrent with, or subsequent to the incorporation, yet prior to the addition of a next complimentary nucleotide; wherein the first, second, third and fourth types of complimentary nucleotides have different mass labels that are attached to the complimentary nucleotides throughout a plurality of cycles of said method for sequencing nucleic acid; and

d) identifying the first type of complimentary nucleotide incorporated in the attached template nucleic acid by detecting a change in the mass dependent property associated with the cantilever, wherein the change is indicative of the incorporation of the first type of complimentary

nucleotide in the attached template nucleic acid.

57. (Previously presented) The method of claim 56, wherein one or more of the first, second, third and fourth types of complimentary nucleotides comprise a chemical structure selected from the group consisting of deoxyadenosine 5' triphosphate (dATP), deoxythymidine 5' triphosphate (dTTP), deoxyguanosine 5' triphosphate (dGTP) and deoxycytosine 5' triphosphate (dCTP).

58. (Previously presented) The method of claim 56, wherein one or more of the first, second, third and fourth types of complimentary nucleotides comprise a chemical structure selected from the group consisting of adenosine 5' triphosphate (ATP), thymidine 5' triphosphate (TTP), guanosine 5' triphosphate (GTP) and cytosine 5' triphosphate (CTP).

59. (Previously presented) The method of claim 56, wherein the change in the mass dependent property of the structure is determined by detecting deflection and/or resonant frequency shifts in the cantilever.

60. (Previously presented) The method of claim 59, wherein the deflection and/or resonant frequency shift is detected by optical beam detection, piezoelectric detection, piezoresistance detection or electrical resistance detection.

61. (Previously presented) The method of claim 56, wherein a single nucleotide

polymorphism (SNP) is identified.

62. (Previously presented) The method of claim 56, further comprising iteratively repeating parts b) through d), wherein for each iteration the attached template is contacted with a different type of complimentary nucleotide.

63. (Previously presented) The method of claim 56, further comprising hybridizing a primer to the attached template nucleic acid.

64. (Previously presented) The method of claim 63, wherein the labeled nucleotides are covalently attached to the 3' end of the primer by a polymerase.

65. (Previously presented) The method of claim 56, wherein the method comprises a plurality of cantilevers, the cantilevers being arranged in a selected pattern.

66. (Currently amended) A method for sequencing nucleic acid, comprising:

a) attaching a template nucleic acid molecule having from about 10 to approximately 100,000 nucleotides in length to a cantilever suitable for detecting a mass dependent property associated with the cantilever, resulting in forming an attached template nucleic acid; wherein the attached template nucleic acid is partially double stranded prior to, concurrent with or subsequent to the attaching of the template nucleic acid;

b) contacting the attached template nucleic acid molecule of a) with at least one type of a

complimentary nucleotide structurally suitable for mass labeling; wherein the complimentary nucleotide optionally comprises a 3' blocking or protecting group;

c) incubating the attached template nucleic acid molecule and the complimentary nucleotide under conditions suitable for incorporating the complimentary nucleotide to the attached template nucleic acid in a position complementary to a nucleotide in the attached template nucleic acid, wherein the complimentary nucleotide incorporated in the attached template nucleic acid is mass labeled prior to, or concurrent with the incorporation, yet prior to the addition of a next complimentary nucleotide; wherein complimentary nucleotides of different types have different mass labels that are attached to the complimentary nucleotides throughout a plurality of cycles of said method for sequencing nucleic acid; and

d) identifying the complimentary nucleotide incorporated in the attached template nucleic acid by detecting a change in the mass dependent property associated with the cantilever, wherein the change is indicative of the incorporation of the complimentary nucleotide in the attached template nucleic acid.

67. (Previously presented) The method of claim 66, wherein the complimentary nucleotide comprises a chemical structure selected from the group consisting of deoxyadenosine 5' triphosphate (dATP), deoxythymidine 5' triphosphate (dTTP), deoxyguanosine 5' triphosphate (dGTP) and deoxycytosine 5' triphosphate (dCTP).

68. (Previously presented) The method of claim 66, wherein the complimentary nucleotide

comprises a chemical structure selected from the group consisting of adenosine 5' triphosphate (ATP), thymidine 5' triphosphate (TTP), guanosine 5' triphosphate (GTP) and cytosine 5' triphosphate (CTP).

69. (Previously presented) The method of claim 66, wherein the change in the mass dependent property of the structure is determined by detecting deflection and/or resonant frequency shifts in the cantilever.

70. (Previously presented) The method of claim 69, wherein the deflection and/or resonant frequency shift is detected by optical beam detection, piezoelectric detection, piezoresistance detection or electrical resistance detection.

71. (Previously presented) The method of claim 66, wherein a single nucleotide polymorphism (SNP) is identified.

72. (Previously presented) The method of claim 66, further comprising iteratively repeating parts b) through d), wherein for each iteration the attached template is contacted with a different type of complimentary nucleotide.

73. (Previously presented) The method of claim 66, further comprising hybridizing a primer to the attached template nucleic acid.

74. (Previously presented) The method of claim 73, wherein the labeled nucleotides are covalently attached to the 3' end of the primer by a polymerase.

75. (Previously presented) The method of claim 66, wherein the method comprises a plurality of cantilevers, the cantilevers being arranged in a selected pattern.

76. (Currently amended) A method for sequencing nucleic acid, comprising:

a) attaching a template nucleic acid molecule having from about 10 to approximately 100,000 nucleotides in length to a cantilever suitable for detecting a mass dependent property associated with the cantilever, resulting in forming an attached template nucleic acid; wherein the attached template nucleic acid is partially double stranded prior to, concurrent with or subsequent to the attaching of the template nucleic acid;

b) contacting the attached template nucleic acid molecule with a first type of complimentary nucleotide structurally suitable for mass labeling, a second type of complimentary nucleotide structurally suitable for mass labeling, a third type of complimentary nucleotide structurally suitable for mass labeling, and a fourth type of complimentary nucleotide structurally suitable for mass labeling; wherein the first, second, third and fourth types of complimentary nucleotides optionally comprise a 3' blocking or protecting group;

c) incubating the attached template nucleic acid molecule and the first, second, third and fourth types of complimentary nucleotides under conditions suitable for incorporating the first type of complimentary nucleotide to the attached template nucleic acid in a position

complementary to a nucleotide in the attached template nucleic acid, wherein the first type of complimentary nucleotide incorporated in the attached template nucleic acid is mass labeled prior to, or concurrent with the incorporation, yet prior to the addition of a next complimentary nucleotide; wherein the first, second, third and fourth types of complimentary nucleotides have different mass labels that are attached to the complimentary nucleotides throughout a plurality of cycles of said method for sequencing nucleic acid; and

d) identifying the first type of complimentary nucleotide incorporated in the attached template nucleic acid by detecting a change in the mass dependent property associated with the cantilever, wherein the change is indicative of the incorporation of the first type of complimentary nucleotide in the attached template nucleic acid.

77. (Previously presented) The method of claim 76, wherein one or more of the first, second, third and fourth types of complimentary nucleotides comprise a chemical structure selected from the group consisting of deoxyadenosine 5' triphosphate (dATP), deoxythymidine 5' triphosphate (dTTP), deoxyguanosine 5' triphosphate (dGTP) and deoxycytosine 5' triphosphate (dCTP).

78. (Previously presented) The method of claim 76, wherein one or more of the first, second, third and fourth types of complimentary nucleotides comprise a chemical structure selected from the group consisting of adenosine 5' triphosphate (ATP), thymidine 5' triphosphate (TTP), guanosine 5' triphosphate (GTP) and cytosine 5' triphosphate (CTP).

79. (Previously presented) The method of claim 76, wherein the change in the mass dependent property of the structure is determined by detecting deflection and/or resonant frequency shifts in the cantilever.

80. (Previously presented) The method of claim 79, wherein the deflection and/or resonant frequency shift is detected by optical beam detection, piezoelectric detection, piezoresistance detection or electrical resistance detection.

81. (Previously presented) The method of claim 76, wherein a single nucleotide polymorphism (SNP) is identified.

82. (Previously presented) The method of claim 76, further comprising iteratively repeating parts b) through d), wherein for each iteration the attached template is contacted with a different type of complimentary nucleotide.

83. (Previously presented) The method of claim 76, further comprising hybridizing a primer to the attached template nucleic acid.

84. (Previously presented) The method of claim 83, wherein the labeled nucleotides are covalently attached to the 3' end of the primer by a polymerase.

85. (Previously presented) The method of claim 76, wherein the method comprises a

plurality of cantilevers, the cantilevers being arranged in a selected pattern.

86. (New) The method of claim 46, wherein the mass labels are selected from the group consisting of nanoparticles, nanoparticle aggregates, carbon nanotubes, fullerenes, functionalized fullerenes, functionalized fullerenes, quantum dots, dendrimers, and combinations thereof.

87. (New) The method of claim 56, wherein the mass labels are selected from the group consisting of nanoparticles, nanoparticle aggregates, carbon nanotubes, fullerenes, functionalized fullerenes, functionalized fullerenes, quantum dots, dendrimers, and combinations thereof.

88. (New) The method of claim 66, wherein the mass labels are selected from the group consisting of nanoparticles, nanoparticle aggregates, carbon nanotubes, fullerenes, functionalized fullerenes, functionalized fullerenes, quantum dots, dendrimers, and combinations thereof.

89. (New) The method of claim 76, wherein the mass labels are selected from the group consisting of nanoparticles, nanoparticle aggregates, carbon nanotubes, fullerenes, functionalized fullerenes, functionalized fullerenes, quantum dots, dendrimers, and combinations thereof.

90. (New) The method of claim 46, wherein a plurality of the complimentary nucleotides having mass labels are removed and replaced with unlabeled nucleotides.

91. (New) The method of claim 56, wherein a plurality of the complimentary nucleotides

having mass labels are removed and replaced with unlabeled nucleotides.

92. (New) The method of claim 66, wherein a plurality of the complimentary nucleotides having mass labels are removed and replaced with unlabeled nucleotides.

93. (New) The method of claim 76, wherein a plurality of the complimentary nucleotides having mass labels are removed and replaced with unlabeled nucleotides.

94. (New) The method of claim 46, wherein the plurality of cycles represent ten cycles.